

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
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Application Serial Number: 10/586,978
Source: I.FWP
Date Processed by STIC: 08/03/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/03/2006

PATENT APPLICATION: US/10/586,978

TIME: 09:46:39

Input Set : F:\SEQLIST.TXT

Output Set: N:\CRF4\08032006\J586978.raw

3 <110> APPLICANT: Kohonen-Corish, Maija
 5 <120> TITLE OF INVENTION: Methods of diagnosing colorectal cancer and reagents therefor

7 <130> FILE REFERENCE: RICE-029
 C--> 9 <140> CURRENT APPLICATION NUMBER: US/10/586,978
 C--> 9 <141> CURRENT FILING DATE: 2006-07-20
 9 <150> PRIOR APPLICATION NUMBER: AU 2004900340
 10 <151> PRIOR FILING DATE: 2004-01-23
 12 <150> PRIOR APPLICATION NUMBER: US 60/540,662
 13 <151> PRIOR FILING DATE: 2004-01-29
 15 <150> PRIOR APPLICATION NUMBER: PCT/AU2005/000077
 16 <151> PRIOR FILING DATE: 2005-01-24
 18 <160> NUMBER OF SEQ ID NOS: 46
 20 <170> SOFTWARE: PatentIn version 3.3
 22 <210> SEQ ID NO: 1
 23 <211> LENGTH: 4181
 24 <212> TYPE: DNA
 25 <213> ORGANISM: Homo sapiens
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (221)..(2707)
 32 <400> SEQUENCE: 1

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37	tgtggcagaa gggaccaagc agtggatatt gagcctgtga agtccaactc ttaagctccg	180
39	agacctgggg gactgagagc ccagctctga aaagtgcac atg aat tcc gga gtt	235
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43	gcc atg aaa tat gga aac gac tcc tcg gcc gag ctg agt gag ctc cat	283
44	Ala Met Lys Tyr Gly Asn Asp Ser Ser Ala Glu Leu Ser Glu Leu His	
45	10 15 20	
47	tca gca gcc ctg gca tca cta aag gga gat ata gtg gaa ctt aat aaa	331
48	Ser Ala Ala Leu Ala Ser Leu Lys Gly Asp Ile Val Glu Leu Asn Lys	
49	25 30 35	
51	cgt ctc cag caa aca gag agg gaa cgg gac ctt ctg gaa aag aaa ttg	379
52	Arg Leu Gln Gln Thr Glu Arg Glu Arg Asp Leu Leu Glu Lys Lys Leu	
53	40 45 50	
55	gcc aag gca cag tgc gag cag tcc cac ctc atg aga gag cat gag gat	427
56	Ala Lys Ala Gln Cys Glu Gln Ser His Leu Met Arg Glu His Glu Asp	
57	55 60 65	
59	gtc cag gag cga acg acg ctt cgc tat gag gaa cgc atc aca gag ctc	475
60	Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu Arg Ile Thr Glu Leu	
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63	cac agc gtc att gcg gag ctc aac aag aag ata gac cgt ctg caa ggc	523

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68 Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu Leu Arg Ser Glu Leu
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71 agc cag agc caa cac gag gtc aac gag gac tct cga agc atg gac caa      619
72 Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser Arg Ser Met Asp Gln
73          120          125          130
75 gac cag acc tct gtc tct atc ccc gaa aac cag tct acc atg gtt act      667
76 Asp Gln Thr Ser Val Ser Ile Pro Glu Asn Gln Ser Thr Met Val Thr
77          135          140          145
79 gct gac atg gac aac tgc agt gac ctg aac tca gaa ctg cag agg gtg      715
80 Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser Glu Leu Gln Arg Val
81 150          155          160          165
83 ctg aca ggg ctg gag aat gtt gtc tgc ggc agg aag aag agc agc tgc      763
84 Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg Lys Lys Ser Ser Cys
85          170          175          180
87 agc ctc tcc gtg gcc gag gtg gac agg cac att gag cag ctc acc aca      811
88 Ser Leu Ser Val Ala Glu Val Asp Arg His Ile Glu Gln Leu Thr Thr
89          185          190          195
91 gcc agc gag cac tgt gac ctg gct att aag aca gtc gag gag att gag      859
92 Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr Val Glu Glu Ile Glu
93          200          205          210
95 ggg gtg ctt ggc cgg gac ctg tat ccc aac ctg gct gaa gag agg tct      907
96 Gly Val Leu Gly Arg Asp Leu Tyr Pro Asn Leu Ala Glu Glu Arg Ser
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99 cgg tgg gag aag gag ctg gct ggg ctg agg gaa gag aat gag agc ctg      955
100 Arg Trp Glu Lys Glu Leu Ala Gly Leu Arg Glu Glu Asn Glu Ser Leu
101 230          235          240          245
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108 Thr Met Asn Ala Ile Arg Glu Glu Arg Asp Arg Leu Arg Arg Arg Val
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111 aga gag ctt caa act cga cta cag agc gtg cag gcc aca ggt ccc tcc      1099
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115 agc cct ggc cgc ctc act tcc acc aac cgc ccg att aac ccc agc act      1147
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123 att gct gag agg gtg aag cta tca aag aca agg tcc gaa tcg tca tca      1243
124 Ile Ala Glu Arg Val Lys Leu Ser Lys Thr Arg Ser Glu Ser Ser Ser
125          330          335          340
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128 Ser Asp Arg Pro Val Leu Gly Ser Glu Ile Ser Ser Ile Gly Val Ser

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133 360 365 370				
135 atc caa gag att ttc caa aca ctc tac tca cac gga tct gcc atc tca	1387			
136 Ile Gln Glu Ile Phe Gln Thr Leu Tyr Ser His Gly Ser Ala Ile Ser				
137 375 380 385				
139 gaa agc aag att aga gag ttt gag gtg gaa aca gaa cgg ctg aat agc	1435			
140 Glu Ser Lys Ile Arg Glu Phe Glu Val Glu Thr Glu Arg Leu Asn Ser				
141 390 395 400 405				
143 cgg att gag cac ctc aaa tcc caa aat gac ctc ctg acc ata acc ttg	1483			
144 Arg Ile Glu His Leu Lys Ser Gln Asn Asp Leu Leu Thr Ile Thr Leu				
145 410 415 420				
147 gag gaa tgt aaa agc aat gct gag agg atg agc atg ctg gtg gga aaa	1531			
148 Glu Glu Cys Lys Ser Asn Ala Glu Arg Met Ser Met Leu Val Gly Lys				
149 425 430 435				
151 tac gaa tcc aat gcc aca gcg ctg agg ctg gcc ttg cag tac agc gag	1579			
152 Tyr Glu Ser Asn Ala Thr Ala Leu Arg Leu Ala Leu Gln Tyr Ser Glu				
153 440 445 450				
155 cag tgc atc gaa gcc tac gaa ctc ctc ctg gcg ctg gca gag agt gag	1627			
156 Gln Cys Ile Glu Ala Tyr Glu Leu Leu Leu Ala Leu Ala Glu Ser Glu				
157 455 460 465				
159 cag agc ctc atc ctg ggg cag ttc cga gcg gcg ggc gtg ggg tcc tcc	1675			
160 Gln Ser Leu Ile Leu Gly Gln Phe Arg Ala Ala Gly Val Gly Ser Ser				
161 470 475 480 485				
163 cct gga gac cag tgc ggg gat gaa aac atc act cag atg ctc aag cga	1723			
164 Pro Gly Asp Gln Ser Gly Asp Glu Asn Ile Thr Gln Met Leu Lys Arg				
165 490 495 500				
167 gct cat gac tgc cgg aag aca gct gag aac gct gcc aag gcc ctg ctc	1771			
168 Ala His Asp Cys Arg Lys Thr Ala Glu Asn Ala Ala Lys Ala Leu Leu				
169 505 510 515				
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177 535 540 545				
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185 570 575 580				
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188 Ala Val Lys Leu Thr Met Leu Glu Leu Glu Ser Ile His Ile Asp Pro				
189 585 590 595				
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204	Leu Glu Leu Lys Leu Ser Thr Arg Glu Ala Gln Glu Gln Ala Tyr Leu	
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208	Val His Ile Glu His Leu Lys Ser Glu Val Glu Glu Gln Lys Glu Gln	
209	665 670 675	
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215	ggc aag gag tgt gct gat gct gcc tcc cca gct ctg tcc cta gct gaa	2347
216	Gly Lys Glu Cys Ala Asp Ala Ala Ser Pro Ala Leu Ser Leu Ala Glu	
217	695 700 705	
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237	775 780 785	
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243	agg atg ctc aag caa aga ata gct ctg cta gag gag gag aac tcc agg	2683
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302 <210> SEQ ID NO: 2

303 <211> LENGTH: 829

304 <212> TYPE: PRT

305 <213> ORGANISM: Homo sapiens

307 <400> SEQUENCE: 2

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322 50 55 60
325 Arg Glu His Glu Asp Val Gln Glu Arg Thr Thr Leu Arg Tyr Glu Glu
326 65 70 75 80
329 Arg Ile Thr Glu Leu His Ser Val Ile Ala Glu Leu Asn Lys Lys Ile
330 85 90 95
333 Asp Arg Leu Gln Gly Thr Thr Ile Arg Glu Glu Asp Glu Tyr Ser Glu
334 100 105 110
337 Leu Arg Ser Glu Leu Ser Gln Ser Gln His Glu Val Asn Glu Asp Ser
338 115 120 125
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342 130 135 140
345 Ser Thr Met Val Thr Ala Asp Met Asp Asn Cys Ser Asp Leu Asn Ser
346 145 150 155 160
349 Glu Leu Gln Arg Val Leu Thr Gly Leu Glu Asn Val Val Cys Gly Arg
350 165 170 175
353 Lys Lys Ser Ser Cys Ser Leu Ser Val Ala Glu Val Asp Arg His Ile
354 180 185 190
357 Glu Gln Leu Thr Thr Ala Ser Glu His Cys Asp Leu Ala Ile Lys Thr
358 195 200 205

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/586,978

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:9; N Pos. 9521

VERIFICATION SUMMARY

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Input Set : F:\SEQLIST.TXT

Output Set: N:\CRF4\08032006\J586978.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2947 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:9467